

THE SKIN MYCOBIOME IN PATIENTS WITH ATOPIC DERMATITIS AND HEALTHY INDIVIDUALS

Z. Bakula¹, P. Decewicz², J. Gawor³, A. Jankowska-Konsur⁴, A. Hryncewicz-Gwóźdź⁴, M. Dyląg⁵, R. Gromadka³, T. Jagielski¹

¹Department of Applied Microbiology, Institute of Microbiology, Faculty of Biology, University of Warsaw, Warsaw, Poland

²Department of Bacterial Genetics, Institute of Microbiology, Faculty of Biology, University of Warsaw, Warsaw, Poland

³DNA Sequencing and Oligonucleotide Synthesis Laboratory, Institute of Biochemistry and Biophysics Polish Academy of Science, Warsaw, Poland

⁴Department of Dermatology, Venereology and Allergology, Faculty of Medicine and Dentistry, Wrocław Medical University, Wrocław, Poland

⁵Institute of Genetics and Microbiology, University of Wrocław, Wrocław, Poland

INTRODUCTION

Atopic dermatitis (AD) is a complex chronic inflammatory disease in which fungi are believed to act as aggravating factors. Thus, analysis of the composition of skin mycoflora is crucial for a better understanding of the etiology of AD.

OBJECTIVE

The aim of the study was to explore the skin mycobiome of AD patients and healthy volunteers using culture-independent metagenomic sequencing.

METHODS

The study included 49 AD patients (24 woman, 25 men; mean age: 31.8 ± 13.1) and 50 healthy individuals (39 woman, 11 men; mean age: 37.8 ± 14.3) recruited between 2017 and 2019 at the Department of Dermatology, Venereology and Allergology, Wroclaw Medical University. Samples from the creases of the elbows (AD patients with acute skin lesions on elbows, $n = 44$ and all healthy individuals) or neck/knee bending (AD patients with no acute lesions on elbows, with lesions on neck/knee bending; $n = 6$) were collected with either a scalpel (AD subjects) or OpSite dressings (Smith & Nephew Education; UK) (healthy individuals; **Fig. 1**). DNA was isolated using GeneMATRIX Environmental DNA & RNA Purification Kit (EurX; Poland). Metagenomic sequencing was performed using primers FungITS1 and FungITS2 (**Fig. 2**), as described previously (Fraczek et al., 2017, J Allergy Clin Immunol. 9:39) at the DNA Sequencing and Oligonucleotide Synthesis Laboratory, Polish Academy of Science.

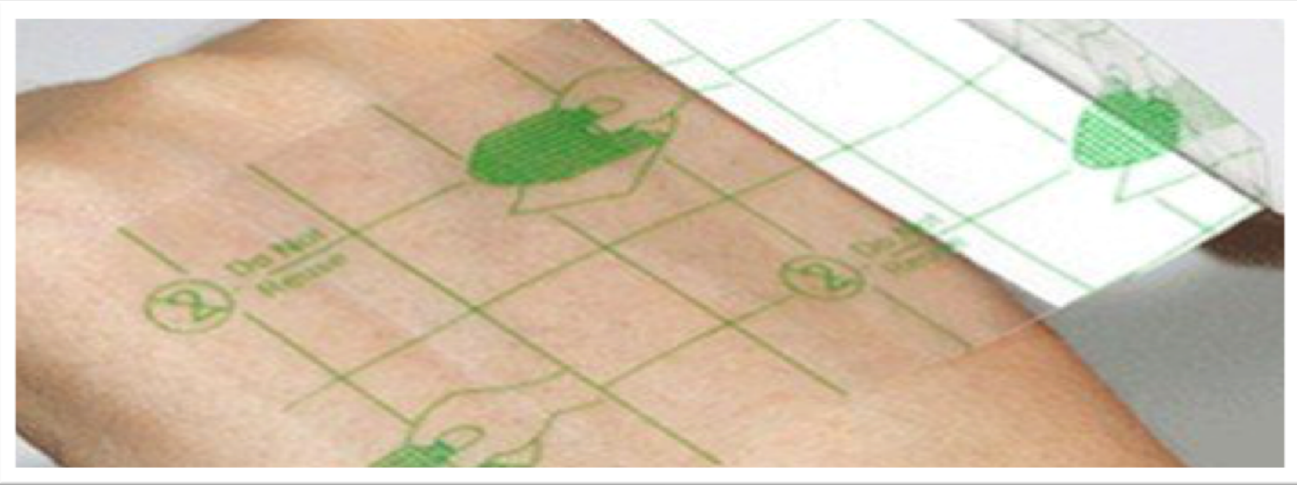


Fig.1 Sample collection. Material from healthy individuals was obtained with an OpSite dressing.

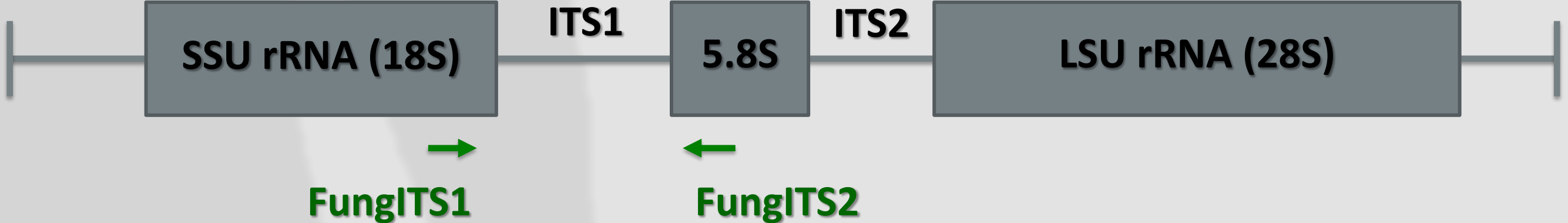


Fig.2 Schematic representation of fungal rDNA operon. Major rRNA genes are shown as boxes. Primers used for PCR amplification are marked in green. SSU, small subunit; LSU, large subunit; ITS, internal transcribed spacer.

RESULTS

A total of **61** and **44** (considering the abundance above 1% within samples) various taxonomic fungal families were found on the skin of AD patients and healthy individuals, respectively. In both groups, the most abundant were fungi of Trichosporonaceae, Cladosporiaceae, Debaryomycetaceae, Malasseziaceae and Saccharomycetales. Among patients with AD, five families, i.e. Cladosporiaceae, Debaryomycetaceae, Malasseziaceae, Saccharomycetales and Botryosphaeriaceae were represented at a higher frequency, when compared with healthy individuals. On the contrary, among healthy subjects Thermoascaceae family was overrepresented.

[illegible]

Table.1 Relative abundance of fungal classes and families in analyzed samples. Samples obtained from AD patients and healthy individuals are in gray- and cream-colored columns, respectively. The shortcuts in taxa names indicate taxa with „Incertae sedis” description („ls”) or taxa that could not be specified at presented taxonomic level („ni”).

CONCLUSIONS

This study provides an important insight into the fungal composition of the skin of AD patients. A higher interpersonal diversity of the mycoflora, and a clear predominance of specific taxa was observed in AD patients when compared with healthy individuals.

This work was supported by the «Iuventus Plus» grant from the Polish Ministry of Science and Higher Education (0258/IP1/2016/74)